

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ni, Jian
Gentz, Reiner L.
Ruben, Steven M.
- (ii) TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
- (iii) NUMBER OF SEQUENCES: 60
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
(B) STREET: 1100 New York Ave., Suite 600
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/028,093
(B) FILING DATE: 09-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Steffe, Eric K.
(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-371-2600
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 52..1020
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTCGGCACGA	GAGCTCTTCT	CACAGGACCA	GCCACTAGCG	CACCTCGAGC	G	ATG	GCC	57
						Met	Ala	
						1		
TAT	GTC	CCC	GCA	CCG	GGC	TAC	CAG	105
Tyr	Val	Pro	Ala	Pro	Gly	Tyr	Gln	
		5				10		
TAC	TAC	CAG	CCC	ATC	CCG	GGC	GGG	153
Tyr	Tyr	Gln	Pro	Ile	Pro	Gly	Gly	
	20					25	Leu	
ATC	CAA	GGA	GTG	GCC	AGC	GAG	CAC	201
Ile	Gln	Gly	Val	Ala	Ser	Glu	His	
35					40		Met	
GTG	GTT	GGG	CAG	GAT	CCG	GGC	TCA	249
Val	Val	Gly	Gln	Asp	Pro	Gly	Ser	
				55			Asp	
CGG	TTT	GAC	GGC	TGG	GAC	AAG	GTG	297
Arg	Phe	Asp	Gly	Trp	Asp	Lys	Val	
			70				75	
AAG	TGG	GGC	AGC	GAG	GAG	AGG	AAG	345
Lys	Trp	Gly	Ser	Glu	Glu	Arg	Lys	
		85					90	
GCC	GCC	TTT	GAG	CTG	GTC	TTC	ATA	393
Ala	Ala	Phe	Glu	Leu	Val	Phe	Ile	
100						105	Val	
GTG	GTA	AAT	GGA	AAT	CCC	TTC	TAT	441
Val	Val	Asn	Gly	Asn	Pro	Phe	Tyr	
115					120		Glu	
CAG	ATG	GTC	ACC	CAC	CTG	CAA	GTG	489
Gln	Met	Val	Thr	His	Leu	Gln	Val	
				135			Asp	
ATC	AAC	TTC	ATC	GGA	GGC	CAG	CCC	537
Ile	Asn	Phe	Ile	Gly	Gly	Gln	Pro	
			150				Leu	
ATG	CCA	CCT	TAC	CCT	GGT	CCC	GGA	585
Met	Pro	Pro	Tyr	Pro	Gly	Pro	Gly	
		165					His	
CTG	CCC	ACC	ATG	GAA	GGA	CCC	CCA	633
Leu	Pro	Thr	Met	Glu	Gly	Pro	Pro	
180						185	Thr	
TTC	GGG	AGG	CTG	CAA	GGA	GGG	CTC	681
Phe	Gly	Arg	Leu	Gln	Gly	Gly	Leu	
195					200		Thr	
AAG	GGC	TAT	GTG	CCT	CCC	ACA	GGC	729
Lys	Gly	Tyr	Val	Pro	Pro	Thr	Gly	
				215			Lys	
GTG	GGC	TCC	TCA	GGG	GAC	ATA	GCT	777
Val	Gly	Ser	Ser	Gly	Asp	Ile	Ala	
			230				Leu	

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 323 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Tyr	Val	Pro	Ala	Pro	Gly	Tyr	Gln	Pro	Thr	Tyr	Asn	Pro	Thr
1				5					10					15	
Leu	Pro	Tyr	Tyr	Gln	Pro	Ile	Pro	Gly	Gly	Leu	Asn	Val	Gly	Met	Ser
			20					25					30		
Val	Tyr	Ile	Gln	Gly	Val	Ala	Ser	Glu	His	Met	Lys	Arg	Phe	Phe	Val
		35					40					45			
Asn	Phe	Val	Val	Gly	Gln	Asp	Pro	Gly	Ser	Asp	Val	Ala	Phe	His	Phe
	50					55					60				
Asn	Pro	Arg	Phe	Asp	Gly	Trp	Asp	Lys	Val	Val	Phe	Asn	Thr	Leu	Gln
	65				70					75					80
Gly	Gly	Lys	Trp	Gly	Ser	Glu	Glu	Arg	Lys	Arg	Ser	Met	Pro	Phe	Lys
				85					90					95	
Lys	Gly	Ala	Ala	Phe	Glu	Leu	Val	Phe	Ile	Val	Leu	Ala	Glu	His	Tyr
			100					105					110		
Lys	Val	Val	Val	Asn	Gly	Asn	Pro	Phe	Tyr	Glu	Tyr	Gly	His	Arg	Leu
		115					120					125			

Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu
130 135 140

Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro
145 150 155 160

Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu
165 170 175

Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val
180 185 190

Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile
195 200 205

Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn
210 215 220

Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg
225 230 235 240

Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp
245 250 255

Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln
260 265 270

Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr
275 280 285

Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe
290 295 300

Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr
305 310 315 320

Val Gln Ile

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16..948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGAGGCGGCG GAGAG ATG GCC TTC AGC GGT TCC CAG GCT CCC TAC CTG AGT	51
Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser	
1 5 10	
CCA GCT GTC CCC TTT TCT GGG ACT ATT CAA GGA GGT CTC CAG GAC GGA	99
Pro Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly	

15				20				25								
CTT Leu	CAG Gln 30	ATC Ile	ACT Thr	GTC Val	AAT Asn 35	GGG Gly	ACC Thr	GTT Val	CTC Leu	AGC Ser	TCC Ser 40	AGT Ser	GGA Gly	ACC Thr	AGG Arg	147
TTT Phe 45	GCT Ala	GTG Val	AAC Asn	TTT Phe	CAG Gln 50	ACT Thr	GGC Gly	TTC Phe	AGT Ser	GGA Gly 55	AAT Asn	GAC Asp	ATT Ile	GCC Ala	TTC Phe 60	195
CAC His	TTC Phe	AAC Asn	CCT Pro	CGG Arg 65	TTT Phe	GAA Glu	GAT Asp	GGA Gly	GGG Gly 70	TAC Tyr	GTG Val	GTG Val	TGC Cys	AAC Asn 75	ACG Thr	243
AGG Arg	CAG Gln	AAC Asn	GGA Gly 80	AGC Ser	TGG Trp	GGG Gly	CCC Pro	GAG Glu 85	GAG Glu	AGG Arg	AAG Lys	ACA Thr	CAC His 90	ATG Met	CCT Pro	291
TTC Phe	CAG Gln	AAG Lys 95	GGG Gly	ATG Met	CCC Pro	TTT Phe	GAC Asp 100	CTC Leu	TGC Cys	TTC Phe	CTG Leu	GTG Val 105	CAG Gln	AGC Ser	TCA Ser	339
GAT Asp 110	TTC Phe	AAG Lys	GTG Val	ATG Met	GTG Val	AAC Asn 115	GGG Gly	ATC Ile	CTC Leu	TTC Phe	GTG Val 120	CAG Gln	TAC Tyr	TTC Phe	CAC His	387
CGC Arg 125	GTG Val	CCC Pro	TTC Phe	CAC His	CGT Arg 130	GTG Val	GAC Asp	ACC Thr	ATC Ile	TCC Ser 135	GTC Val	AAT Asn	GGC Gly	TCT Ser	GTG Val 140	435
CAG Gln	CTG Leu	TCC Ser	TAC Tyr	ATC Ile 145	AGC Ser	TTC Phe	CAG Gln	ACC Thr	CAG Gln 150	ACA Thr	GTC Val	ATC Ile	CAC His	ACA Thr 155	GTG Val	483
CAG Gln	AGC Ser	GCC Ala	CCT Pro 160	GGA Gly	CAG Gln	ATG Met	TTC Phe	TCT Ser 165	ACT Thr	CCC Pro	GCC Ala	ATC Ile	CCA Pro 170	CCT Pro	ATG Met	531
ATG Met	TAC Tyr 175	CCC Pro	CAC His	CCC Pro	GCC Ala	TAT Tyr	CCG Pro 180	ATG Met	CCT Pro	TTC Phe	ATC Ile 185	ACC Thr	ACC Thr	ATT Ile	CTG Leu	579
GGA Gly 190	GGG Gly	CTG Leu	TAC Tyr	CCA Pro	TCC Ser	AAG Lys 195	TCC Ser	ATC Ile	CTC Leu	CTG Leu	TCA Ser 200	GGC Gly	ACT Thr	GTC Val	CTG Leu	627
CCC Pro 205	AGT Ser	GCT Ala	CAG Gln	AGG Arg	TTC Phe 210	CAC His	ATC Ile	AAC Asn	CTG Leu	TGC Cys 215	TCT Ser	GGG Gly	AAC Asn	CAC His	ATC Ile 220	675
GCC Ala	TTC Phe	CAC His	CTG Leu	AAC Asn 225	CCC Pro	CGT Arg	TTT Phe	GAT Asp	GAG Glu 230	AAT Asn	GCT Ala	GTG Val	GTC Val	CGC Arg 235	AAC Asn	723
ACC Thr	CAG Gln	ATC Ile	GAC Asp 240	AAC Asn	TCC Ser	TGG Trp	GGG Gly	TCT Ser 245	GAG Glu	GAG Glu	CGA Arg	AGT Ser	CTG Leu 250	CCC Pro	CGA Arg	771
AAA Lys	ATG Met	CCC Pro 255	TTC Phe	GTC Val	CGT Arg	GGC Gly	CAG Gln 260	AGC Ser	TTC Phe	TCA Ser	GTG Val	TGG Trp 265	ATC Ile	TTG Leu	TGT Cys	819
GAA	GCT	CAC	TGC	CTC	AAG	GTG	GCC	GTG	GAT	GGT	CAG	CAC	CTG	TTT	GAA	867

Glu	Ala	His	Cys	Leu	Lys	Val	Ala	Val	Asp	Gly	Gln	His	Leu	Phe	Glu	
270						275					280					
TAC	TAC	CAT	CGC	CTG	AGG	AAC	CTG	CCC	ACC	ATC	AAC	AGA	CTG	GAA	GTG	915
Tyr	Tyr	His	Arg	Leu	Arg	Asn	Leu	Pro	Thr	Ile	Asn	Arg	Leu	Glu	Val	
285					290					295				300		
GGG	GGC	GAC	ATC	CAG	CTG	ACC	CAT	GTG	CAG	ACA	TAGGCGGCTT	CCTGGCCCTG				968
Gly	Gly	Asp	Ile	Gln	Leu	Thr	His	Val	Gln	Thr						
				305					310							
GGGCCGGGGG	CTGGGGTGTG	GGGCAGTCTG	GGTCCTCTCA	TCATCCCCAC	TTCCCAGGCC											1028
CAGCCTTTCC	AACCCTGCCT	GGGATCTGGG	CTTTAATGCA	GAGGCCATGT	CCTTGTCTGG											1088
TCCTGCTTCT	GGCTACAGCC	ACCCTGGAAC	GGAGAAGGCA	GCTGACGGGG	ATTGCCTTCC											1148
TCAGCCGCAG	CAGCACCTGG	GGCTCCAGCT	GCTGGAAATC	CTACCATCCC	AGGAGGCAGG											1208
CACAGCCAGG	GAGAGGGGAG	GAGTGGGCAG	TGAAGATGAA	GCCCCATGCT	CAGTCCCCTC											1268
CCATCCCCCA	CGCAGCTCCA	CCCCAGTCCC	AAGCCACCAG	CTGTCTGCTC	CTGGTGGGAG											1328
GTGGCCTCCT	CAGCCCCTCC	TCTCTGACCT	TTAACCTCAC	TCTCACCTTG	CACCGTGCAC											1388
CAACCCTTCA	CCCCTCCTGG	AAAGCAGGCC	TGATGGCTTC	CCACTGGCCT	CCACCACCTG											1448
ACCAGAGTGT	TCTCTTCAGA	GGACTGGCTC	CTTTCCCAGT	GTCCTTAAAA	TAAAGAAATG											1508
AAAATGCTTG	TTGGCAAAAA	AAAAAAAAAA	AAAAAAA													1545

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Phe	Ser	Gly	Ser	Gln	Ala	Pro	Tyr	Leu	Ser	Pro	Ala	Val	Pro	
1				5					10					15		
Phe	Ser	Gly	Thr	Ile	Gln	Gly	Gly	Leu	Gln	Asp	Gly	Leu	Gln	Ile	Thr	
		20					25						30			
Val	Asn	Gly	Thr	Val	Leu	Ser	Ser	Ser	Gly	Thr	Arg	Phe	Ala	Val	Asn	
		35					40					45				
Phe	Gln	Thr	Gly	Phe	Ser	Gly	Asn	Asp	Ile	Ala	Phe	His	Phe	Asn	Pro	
	50					55					60					
Arg	Phe	Glu	Asp	Gly	Gly	Tyr	Val	Val	Cys	Asn	Thr	Arg	Gln	Asn	Gly	
65				70					75					80		
Ser	Trp	Gly	Pro	Glu	Arg	Lys	Thr	His	Met	Pro	Phe	Gln	Lys	Gly		
			85				90						95			
Met	Pro	Phe	Asp	Leu	Cys	Phe	Leu	Val	Gln	Ser	Ser	Asp	Phe	Lys	Val	
			100				105						110			

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
115 120 125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
130 135 140

Ile Ser Phe Gln Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro
145 150 155 160

Gly Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His
165 170 175

Pro Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr
180 185 190

Pro Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln
195 200 205

Arg Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu
210 215 220

Asn Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp
225 230 235 240

Asn Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe
245 250 255

Val Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys
260 265 270

Leu Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg
275 280 285

Leu Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile
290 295 300

Gln Leu Thr His Val Gln Thr
305 310

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 118..1068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACACCACTCT TTGGGGCCAG TGCCTCAGTT TCAATCCAGG TAACCTTTAA ATGAAACTTG	60
CCTAAAATCT TAGGTCATAC ACAGAAGAGA CTCCAATCGA CAAGAAGCTG GAAAAGA	117
ATG ATG TTG TCC TTA AAC AAC CTA CAG AAT ATC ATC TAT AAC CCG GTA	165
Met Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val	

1	5	10	15	
ATC CCG TTT GTT GGC ACC ATT CCT GAT CAG CTG GAT CCT GGA ACT TTG Ile Pro Phe Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu 20 25 30				213
ATT GTG ATA CGT GGG CAT GTT CCT AGT GAC GCA GAC AGA TTC CAG GTG Ile Val Ile Arg Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val 35 40 45				261
GAT CTG CAG AAT GGC AGC AGT GTG AAA CCT CGA GCC GAT GTG GCC TTT Asp Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp Val Ala Phe 50 55 60				309
CAT TTC AAT CCT CGT TTC AAA AGG GCC GGC TGC ATT GTT TGC AAT ACT His Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr 65 70 75 80				357
TTG ATA AAT GAA AAA TGG GGA CGG GAA GAG ATC ACC TAT GAC ACG CCT Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro 85 90 95				405
TTC AAA AGA GAA AAG TCT TTT GAG ATC GTG ATT ATG GTG CTA AAG GAC Phe Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp 100 105 110				453
AAA TTC CAG GTG GCT GTA AAT GGA AAA CAT ACT CTG CTC TAT GGC CAC Lys Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly His 115 120 125				501
AGG ATC GGC CCA GAG AAA ATA GAC ACT CTG GGC ATT TAT GGC AAA GTG Arg Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys Val 130 135 140				549
AAT ATT CAC TCA ATT GGT TTT AGC TTC AGC TCG GAC TTA CAA AGT ACC Asn Ile His Ser Ile Gly Phe Ser Phe Ser Ser Asp Leu Gln Ser Thr 145 150 155 160				597
CAA GCA TCT AGT CTG GAA CTG ACA GAG ATA GTT AGA GAA AAT GTT CCA Gln Ala Ser Ser Leu Glu Leu Thr Glu Ile Val Arg Glu Asn Val Pro 165 170 175				645
AAG TCT GGC ACG CCC CAG CTT AGC CTG CCA TTC GCT GCA AGG TTG AAC Lys Ser Gly Thr Pro Gln Leu Ser Leu Pro Phe Ala Ala Arg Leu Asn 180 185 190				693
ACC CCC ATG GGC CCT GGA CGA ACT GTC GTC GTT AAA GGA GAA GTG AAT Thr Pro Met Gly Pro Gly Arg Thr Val Val Val Lys Gly Glu Val Asn 195 200 205				741
GCA AAT GCC AAA AGC TTT AAT GTT GAC CTA CTA GCA GGA AAA TCA AAG Ala Asn Ala Lys Ser Phe Asn Val Asp Leu Leu Ala Gly Lys Ser Lys 210 215 220				789
GAT ATT GCT CTA CAC TTG AAC CCA CGC CTG AAT ATT AAA GCA TTT GTG Asp Ile Ala Leu His Leu Asn Pro Arg Leu Asn Ile Lys Ala Phe Val 225 230 235 240				837
AGA AAT TCT TTT CTT CAA GAG TCC TGG GGA GAA GAA GAG AGA AAT ATT Arg Asn Ser Phe Leu Gln Glu Ser Trp Gly Glu Glu Glu Arg Asn Ile 245 250 255				885
ACC GCT TTC CCA TTT AGT CCT GGG ATG TAC TTT GAG ATG ATA ATT TAT				933

09263600 030500

Thr	Ala	Phe	Pro	Phe	Ser	Pro	Gly	Met	Tyr	Phe	Glu	Met	Ile	Ile	Tyr		
			260					265					270				
TGT	GAT	GTT	AGA	GAA	TTC	AAG	GTT	GCA	GTA	AAT	GGC	GTA	CAC	AGC	CTG	981	
Cys	Asp	Val	Arg	Glu	Phe	Lys	Val	Ala	Val	Asn	Gly	Val	His	Ser	Leu		
		275					280				285						
GAG	TAC	AAA	CAC	AGA	TTT	AAA	GAG	CTC	AGC	AGT	ATT	GAC	ACG	CTG	GAA	1029	
Glu	Tyr	Lys	His	Arg	Phe	Lys	Glu	Leu	Ser	Ser	Ile	Asp	Thr	Leu	Glu		
	290					295					300						
ATT	AAT	GGA	GAC	ATC	CAC	TTA	CTG	GAA	GTA	AGG	AGC	TGG	TAGCCTACCT			1078	
Ile	Asn	Gly	Asp	Ile	His	Leu	Leu	Glu	Val	Arg	Ser	Trp					
305					310					315							
ACACAGCTGC	TACAAAAACC	AAAATACAGA	ATGGCTTCTG	TGATACTGGC	CTTGCTGAAA											1138	
CGCATCTCAC	TGTCATTCTA	TTGTTTATAT	TGTTAAATG	AGCTTGTGCA	CCATTAGGTC											1198	
CTGCTGGGTG	TTCTCAGTCC	TTGCCATGAA	GTATGGTGGT	GTCTAGCACT	GAATGGGGAA											1258	
ACTGGGGGCA	GCAACACTTA	TAGCCAGTTA	AAGCCACTCT	GCCCTCTCTC	CTACTTTGGC											1318	
TGACTCTTCA	AGAATGCCAT	TCAACAAGTA	TTTATGGAGT	CCTACTATAT	ACAGTAGCTA											1378	
ACATGTATTG	AGCACAGATT	TTTTTGGTAA	ACCTGTGAGG	GCTAGGGTAT	ATCCTTGGGA											1438	
ACAAACCAGA	ATGTCCTGTC	CCTTGAAAAA	AAAAAAAAAA	A												1479	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Met	Leu	Ser	Leu	Asn	Asn	Leu	Gln	Asn	Ile	Ile	Tyr	Asn	Pro	Val		
1				5				10						15			
Ile	Pro	Phe	Val	Gly	Thr	Ile	Pro	Asp	Gln	Leu	Asp	Pro	Gly	Thr	Leu		
			20					25					30				
Ile	Val	Ile	Arg	Gly	His	Val	Pro	Ser	Asp	Ala	Asp	Arg	Phe	Gln	Val		
			35				40					45					
Asp	Leu	Gln	Asn	Gly	Ser	Ser	Val	Lys	Pro	Arg	Ala	Asp	Val	Ala	Phe		
	50					55					60						
His	Phe	Asn	Pro	Arg	Phe	Lys	Arg	Ala	Gly	Cys	Ile	Val	Cys	Asn	Thr		
	65				70					75					80		
Leu	Ile	Asn	Glu	Lys	Trp	Gly	Arg	Glu	Glu	Ile	Thr	Tyr	Asp	Thr	Pro		
				85				90						95			
Phe	Lys	Arg	Glu	Lys	Ser	Phe	Glu	Ile	Val	Ile	Met	Val	Leu	Lys	Asp		
			100					105					110				
Lys	Phe	Gln	Val	Ala	Val	Asn	Gly	Lys	His	Thr	Leu	Leu	Tyr	Gly	His		

(2) INFORMATION FOR SEQ ID NO:7:

(A) LENGTH: 1936 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: CDS
(B) LOCATION: 118..717

ACACCAGTCT	TTGGGGCCAG	TGCCTCAGTT	TCAATCCAGG	TAACCTTTAA	ATGAAACTTG	60
CCTAAAATCT	TAGGTCATAC	ACAGAAGAGA	CTCCAATCGA	CAAGAAGCTG	GAAAAGA	117
ATG ATG TTG TCC TTA AAC AAC CTA CAG AAT ATC ATC TAT AAC CCG GTA	165					
Met Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val						
1 5 10 15						

ATC	CCG	TTT	GTT	GGC	ACC	ATT	CCT	GAT	CAG	CTG	GAT	CCT	GGA	ACT	TTG		213
Ile	Pro	Phe	Val	Gly	Thr	Ile	Pro	Asp	Gln	Leu	Asp	Pro	Gly	Thr	Leu		
			20					25					30				
ATT	GTG	ATA	CGT	GGG	CAT	GTT	CCT	AGT	GAC	GCA	GAC	AGA	TTC	CAG	GTG		261
Ile	Val	Ile	Arg	Gly	His	Val	Pro	Ser	Asp	Ala	Asp	Arg	Phe	Gln	Val		
		35					40					45					
GAT	CTG	CAG	AAT	GGC	AGC	AGC	ATG	AAA	CCT	CGA	GCC	GAT	GTG	GCC	TTT		309
Asp	Leu	Gln	Asn	Gly	Ser	Ser	Met	Lys	Pro	Arg	Ala	Asp	Val	Ala	Phe		
	50					55					60						
CAT	TTC	AAT	CCT	CGT	TTC	AAA	AGG	GCC	GGC	TGC	ATT	GTT	TGC	AAT	ACT		357
His	Phe	Asn	Pro	Arg	Phe	Lys	Arg	Ala	Gly	Cys	Ile	Val	Cys	Asn	Thr		
	65				70				75						80		
TTG	ATA	AAT	GAA	AAA	TGG	GGA	CGG	GAA	GAG	ATC	ACC	TAT	GAC	ACG	CCT		405
Leu	Ile	Asn	Glu	Lys	Trp	Gly	Arg	Glu	Glu	Ile	Thr	Tyr	Asp	Thr	Pro		
			85					90						95			
TTC	AAA	AGA	GAA	AAG	TCT	TTT	GAG	ATC	GTG	ATT	ATG	GTG	CTG	AAG	GAC		453
Phe	Lys	Arg	Glu	Lys	Ser	Phe	Glu	Ile	Val	Ile	Met	Val	Leu	Lys	Asp		
			100				105						110				
AAA	TTC	CAG	GTG	GCT	GTA	AAT	GGA	AAA	CAT	ACT	CTG	CTC	TAT	GGC	CAC		501
Lys	Phe	Gln	Val	Ala	Val	Asn	Gly	Lys	His	Thr	Leu	Leu	Tyr	Gly	His		
		115					120					125					
AGG	ATC	GGC	CCA	GAG	AAA	ATA	GAC	ACT	CTG	GGC	ATT	TAT	GGC	AAA	GTG		549
Arg	Ile	Gly	Pro	Glu	Lys	Ile	Asp	Thr	Leu	Gly	Ile	Tyr	Gly	Lys	Val		
	130					135					140						
AAT	ATT	CAC	TCA	ATT	GGT	TTT	AGC	TTC	AGC	TCG	GAC	TTA	CAA	AGT	ACC		597
Asn	Ile	His	Ser	Ile	Gly	Phe	Ser	Phe	Ser	Ser	Asp	Leu	Gln	Ser	Thr		
	145				150				155						160		
CAA	GCA	TCT	AGT	CTG	GAA	CTG	ACA	GAG	ATA	AGT	AGA	GAA	AAT	GTT	CCA		645
Gln	Ala	Ser	Ser	Leu	Glu	Leu	Thr	Glu	Ile	Ser	Arg	Glu	Asn	Val	Pro		
				165				170						175			
AAG	TCT	GGC	ACG	CCC	CAG	CTT	GTG	AGT	ATT	TTT	GCC	TGG	GTT	ATT	TCA		693
Lys	Ser	Gly	Thr	Pro	Gln	Leu	Val	Ser	Ile	Phe	Ala	Trp	Val	Ile	Ser		
			180				185						190				
TGT	GGA	ATA	TTT	TAT	AAA	GTT	GCA	TAGAAAATGA	ACAGTTTAAA	CCGTGGAGGG							747
Cys	Gly	Ile	Phe	Tyr	Lys	Val	Ala										
		195				200											
CAGCTTCATT	CATTCCATT	CTTACTGTAG	AACTGTTTTCC	CTACAGCCTA	GTAATAGAGG												807
AGGAGACATT	TCTAAAATCG	CACCCAGAAC	TGTCTACACC	AAGAGCAAAG	ATTCGACTGT												867
CAATCACACT	TTGACTTGCA	CCAAAATACC	ACCTATGAAC	TATGTGTCAA	AGGGTT												

TCATCGTCTA AAATGTAATC ATGTGTGTTT GCTTCGAGCC AGGGACAGTG CTGCTGCAGG 1287
GGACCCAGCT GGGACCAAGG CAGACTGTCT CTCCCCTCCT GGGATTTACA GGGTCATGGC 1347
TCTGAAACAT TCCGTAGTGT TCTTTGGACA CGAGTTTTCC CTGGAGATCG CTTTCTGCAG 1407
GCTCTTGCTC CTGACTGTGG CTTCTTTTCA GAGGCTGCCA TTTCGCTGCA AGGTTGAACA 1467
CCCCCATGGG CCCTGGACGA ACTGTCGTCG TTAAAGGAGA AGTGAATGCA AATGCCAAAA 1527
GCTTTAATGT TGACCTACTA GCAGGAAAAT CAAAGGATAT TGCTCTACAC TTGAACCCAC 1587
GCCTGAATAT TAAAGCATTT GTAAGAAATT CTTTCTTCA GGAGTCCTGG GGAGAAGAAG 1647
AGAGAAATAT TACCTCTTTC CCATTTAGTC CTGGGATGTA CTTTGAGATG ATAATTTATT 1707
GTGATGTTAG AGAATTCAAG GTTGCAAGTAA ATGGCGTACA CAGCCTGGAG TACAAACACA 1767
GATTTAAAGA GCTCAGCAGT ATTGACACGC TGGAAATTAA TGGAGACATC CACTTACTGG 1827
AAGTAAGGAG CTGGTAGCCT ACCTACACAG CTGCTACAAA AACCAAATA CAGAATGGCT 1887
TCTGTGATAC TGGCCTTGCT GAAACGCAAA AAAAAAAAAA AAAAAAAAAA 1936

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val
1 5 10 15
Ile Pro Phe Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr Leu
20 25 30
Ile Val Ile Arg Gly His Val Pro Ser Asp Ala Asp Arg Phe Gln Val
35 40 45
Asp Leu Gln Asn Gly Ser Ser Met Lys Pro Arg Ala Asp Val Ala Phe
50 55 60
His Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile Val Cys Asn Thr
65 70 75 80
Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile Thr Tyr Asp Thr Pro
85 90 95
Phe Lys Arg Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asp
100 105 110
Lys Phe Gln Val Ala Val Asn Gly Lys His Thr Leu Leu Tyr Gly His
115 120 125
Arg Ile Gly Pro Glu Lys Ile Asp Thr Leu Gly Ile Tyr Gly Lys Val
130 135 140

(2) INFORMATION FOR SEQ ID NO:9:

(A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

(2) INFORMATION FOR SEQ ID NO:10:

(A) LENGTH: 250 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Met 1	Ala	Asp	Asn 5	Phe	Ser	Leu	His	Asp	Ala 10	Leu	Ser	Gly	Ser	Gly 15	Asn
Pro	Asn	Pro	Gln 20	Gly	Trp	Pro	Gly	Ala 25	Trp	Gly	Asn	Gln	Pro 30	Ala	Gly
Ala	Gly	Gly 35	Tyr	Pro	Gly	Ala	Ser 40	Tyr	Pro	Gly	Ala	Tyr 45	Pro	Gly	Gln
Ala	Pro 50	Pro	Gly	Ala	Tyr	Pro 55	Gly	Gln	Ala	Pro	Pro 60	Gly	Ala	Tyr	His
Gly 65	Ala	Pro	Gly	Ala	Tyr 70	Pro	Gly	Ala	Pro	Ala 75	Pro	Gly	Val	Tyr	Pro 80
Gly	Pro	Pro	Ser	Gly 85	Pro	Gly	Ala	Tyr	Pro 90	Ser	Ser	Gly	Gln	Pro 95	Ser
Ala	Pro	Gly	Ala 100	Tyr	Pro	Ala	Thr	Gly 105	Pro	Tyr	Gly	Ala	Pro 110	Ala	Gly
Pro	Leu	Ile 115	Val	Pro	Tyr	Asn	Leu 120	Pro	Leu	Pro	Gly	Gly 125	Val	Val	Pro
Arg	Met 130	Leu	Ile	Thr	Ile	Leu 135	Gly	Thr	Val	Lys	Pro 140	Asn	Ala	Asn	Arg
Ile 145	Ala	Leu	Asp	Phe	Gln 150	Arg	Gly	Asn	Asp	Val 155	Ala	Phe	His	Phe	Asn 160
Pro	Arg	Phe	Asn	Glu 165	Asn	Asn	Arg	Arg	Val 170	Ile	Val	Cys	Asn	Thr 175	Lys
Leu	Asp	Asn	Asn 180	Trp	Gly	Arg	Glu	Glu 185	Arg	Gln	Ser	Val	Phe 190	Pro	Phe
Glu	Ser	Gly 195	Lys	Pro	Phe	Lys	Ile 200	Gln	Val	Leu	Val	Glu 205	Pro	Asp	His
Phe	Lys 210	Val	Ala	Val	Asn	Asp 215	Ala	His	Leu	Leu	Gln 220	Tyr	Asn	His	Arg
Val 225	Lys	Lys	Leu	Asn	Glu 230	Ile	Ser	Lys	Leu	Gly 235	Ile	Ser	Gly	Asp	Ile 240
Asp	Leu	Thr	Ser	Ala 245	Ser	Tyr	Thr	Met	Ile 250						

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

Met 1	Ala	Tyr	Val 5	Pro	Ala	Pro	Gly	Tyr	Gln 10	Pro	Thr	Tyr	Asn	Pro 15	Thr
Leu	Pro	Tyr	Lys 20	Arg	Pro	Ile	Pro	Gly 25	Gly	Leu	Ser	Val	Gly 30	Met	Ser
Ile	Tyr	Ile 35	Gln	Gly	Ile	Ala	Lys 40	Asp	Asn	Met	Arg	Arg 45	Phe	His	Val
Asn	Phe 50	Ala	Val	Gly	Gln	Asp 55	Glu	Gly	Ala	Asp	Ile 60	Ala	Phe	His	Phe
Asn 65	Pro	Arg	Phe	Asp	Gly 70	Trp	Asp	Lys	Val	Val 75	Phe	Asn	Thr	Met	Gln 80
Ser	Gly	Gln	Trp 85	Gly	Lys	Glu	Glu	Lys	Lys 90	Lys	Ser	Met	Pro	Phe 95	Gln
Lys	Gly	His	His 100	Phe	Glu	Leu	Val	Phe 105	Met	Val	Met	Ser	Glu 110	His	Tyr
Lys	Val	Val 115	Val	Asn	Gly	Thr	Pro 120	Phe	Tyr	Glu	Tyr	Gly 125	His	Arg	Leu
Pro	Leu 130	Gln	Met	Val	Thr	His 135	Leu	Gln	Val	Asp	Gly 140	Asp	Leu	Glu	Leu
Gln 145	Ser	Ile	Asn	Phe	Leu 150	Gly	Gly	Gln	Pro	Ala 155	Ala	Ser	Gln	Tyr	Pro 160
Gly	Thr	Met	Thr	Ile 165	Pro	Ala	Tyr	Pro	Ser 170	Ala	Gly	Tyr	Asn	Pro 175	Pro
Gln	Met	Asn	Ser 180	Leu	Pro	Val	Met	Ala 185	Gly	Pro	Pro	Ile	Phe 190	Asn	Pro
Pro	Val 195	Pro	Tyr	Val	Gly	Thr	Leu 200	Gln	Gly	Gly	Leu	Thr 205	Ala	Arg	Arg
Thr	Ile 210	Ile	Ile	Lys	Gly	Tyr 215	Val	Leu	Pro	Thr	Ala 220	Lys	Asn	Leu	Ile
Ile 225	Asn	Phe	Lys	Val	Gly 230	Ser	Thr	Gly	Asp	Ile 235	Ala	Phe	His	Met	Asn 240
Pro	Arg	Ile	Gly	Asp 245	Cys	Val	Val	Arg	Asn 250	Ser	Tyr	Met	Asn	Gly 255	Ser
Trp	Gly	Ser	Glu 260	Glu	Arg	Lys	Ile	Pro 265	Tyr	Asn	Pro	Phe	Gly 270	Ala	Gly
Gln	Phe 275	Phe	Asp	Leu	Ser	Ile	Arg 280	Cys	Gly	Thr	Asp	Arg 285	Phe	Lys	Val
Phe	Ala 290	Asn	Gly	Gln	His	Leu 295	Phe	Asp	Phe	Ser	His 300	Arg	Phe	Gln	Ala
Phe 305	Gln	Arg	Val	Asp	Met 310	Leu	Glu	Ile	Lys	Gly 315	Asp	Ile	Thr	Leu	Ser 320

Tyr Val Gln Ile

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

[illegible]

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ser	Asn	Val	Pro	His	Lys	Ser	Ser	Leu	Pro	Glu	Gly	Ile	Arg	Pro
1				5					10					15	
Gly	Thr	Val	Leu	Arg	Ile	Arg	Gly	Leu	Val	Pro	Pro	Asn	Ala	Ser	Arg
		20						25					30		
Phe	His	Val	Asn	Leu	Leu	Cys	Gly	Glu	Glu	Gln	Gly	Ser	Asp	Ala	Ala
		35					40					45			
Leu	His	Phe	Asn	Pro	Arg	Leu	Asp	Thr	Ser	Glu	Val	Val	Phe	Asn	Ser
	50					55					60				
Lys	Glu	Gln	Gly	Ser	Trp	Gly	Arg	Glu	Glu	Arg	Gly	Pro	Gly	Val	Pro
65					70					75					80
Phe	Gln	Arg	Gly	Gln	Pro	Phe	Glu	Val	Leu	Ile	Ile	Ala	Ser	Asp	Asp
				85					90					95	
Gly	Phe	Lys	Ala	Val	Val	Gly	Asp	Ala	Gln	Tyr	His	His	Phe	Arg	His
			100					105					110		
Arg	Leu	Pro	Leu	Ala	Arg	Val	Arg	Leu	Val	Glu	Val	Gly	Gly	Asp	Val
		115					120					125			
Gln	Leu	Asp	Ser	Val	Arg	Ile	Phe								
	130					135									

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Asp	Gly	Phe	Ser	Leu	Asn	Asp	Ala	Leu	Ala	Gly	Ser	Gly	Asn
1				5					10					15	
Pro	Asn	Pro	Gln	Gly	Trp	Pro	Gly	Ala	Trp	Gly	Asn	Gln	Pro	Gly	Ala
		20						25					30		
Gly	Gly	Tyr	Pro	Gly	Ala	Ser	Tyr	Pro	Gly	Ala	Tyr	Pro	Gly	Gln	Ala
		35					40					45			
Pro	Pro	Gly	Gly	Tyr	Pro	Gly	Gln	Ala	Pro	Pro	Ser	Ala	Tyr	Pro	Gly
	50					55					60				
Pro	Thr	Gly	Pro	Ser	Ala	Tyr	Pro	Gly	Pro	Thr	Ala	Pro	Gly	Ala	Tyr
65					70					75					80
Pro	Gly	Pro	Thr	Ala	Pro	Gly	Ala	Phe	Pro	Gly	Gln	Pro	Gly	Gly	Pro
				85				90					95		
Gly	Ala	Tyr	Pro	Ser	Ala	Pro	Gly	Ala	Tyr	Pro	Ser	Ala	Pro	Gly	Ala
			100					105					110		

Arg Lys Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asn Lys
100 105 110

Phe His Val Ala Val Asn Gly Lys His Ile Leu Leu Tyr Ala His Arg
115 120 125

Ile Asn Pro Glu Lys Ile Asp Thr Leu Gly Ile Phe Gly Lys Val Asn
130 135 140

Ile His Ser Ile Gly Phe Arg Phe Ser Ser Asp Leu Gln Ser Met Glu
145 150 155 160

Thr Ser Thr Leu Gly Leu Thr Gln Ile Ser Lys Glu Asn Ile Gln Lys
165 170 175

Ser Gly Lys Leu His Leu Ser Leu Pro Phe Glu Ala Arg Leu Asn Ala
180 185 190

Ser Met Gly Pro Gly Arg Thr Val Val Val Lys Gly Glu Val Asn Thr
195 200 205

Asn Ala Thr Ser Phe Asn Val Asp Leu Val Ala Gly Arg Ser Arg Asp
210 215 220

Ile Ala Leu His Leu Asn Pro Arg Leu Asn Val Lys Ala Phe Val Arg
225 230 235 240

Asn Ser Phe Leu Gln Asp Ala Trp Gly Glu Glu Glu Arg Asn Ile Thr
245 250 255

Cys Phe Pro Phe Ser Ser Gly Met Tyr Phe Glu Met Ile Ile Tyr Cys
260 265 270

Asp Val Arg Glu Phe Lys Val Ala Val Asn Gly Val His Ser Leu Glu
275 280 285

Tyr Lys His Arg Phe Lys Asp Leu Ser Ser Ile Asp Thr Leu Ala Val
290 295 300

Asp Gly Asp Ile Arg Leu Leu Asp Val Arg Ser Trp
305 310 315

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu
1 5 10 15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val
20 25 30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro
35 40 45
Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys
50 55 60
Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe
65 70 75 80
Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn
85 90 95
Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg
100 105 110
Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys
115 120 125
Ile Lys Cys Val Ala Phe Asp
130 135

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Leu Ser Leu Ser Asn Leu Gln Asn Ile Ile Tyr Asn Pro Thr Ile
1 5 10 15
Pro Tyr Val Ser Thr Ile Thr Glu Gln Leu Lys Pro Gly Ser Leu Ile
20 25 30
Val Ile Arg Gly His Val Pro Lys Asp Ser Glu Arg Phe Gln Val Asp
35 40 45
Phe Gln His Gly Asn Ser Leu Lys Pro Arg Ala Asp Val Ala Phe His
50 55 60
Phe Asn Pro Arg Phe Lys Arg Ser Asn Cys Ile Val Cys Asn Thr Leu
65 70 75 80
Thr Asn Glu Lys Trp Gly Trp Glu Glu Ile Thr His Asp Met Pro Phe
85 90 95
Arg Lys Glu Lys Ser Phe Glu Ile Val Ile Met Val Leu Lys Asn Lys
100 105 110
Phe His Val Ala Val Asn Gly Lys His Ile Leu Leu Tyr Ala His Arg
115 120 125
Ile Asn Pro Glu Lys Ile Asp Thr Leu Gly Ile Phe Gly Lys Val Asn
130 135 140

Ile	His	Ser	Ile	Gly	Phe	Arg	Phe	Ser	Ser	Asp	Leu	Gln	Ser	Met	Glu
145					150					155					160
Thr	Ser	Thr	Leu	Gly	Leu	Thr	Gln	Ile	Ser	Lys	Glu	Asn	Ile	Gln	Lys
				165					170					175	
Ser	Gly	Lys	Leu	His	Leu	Ser	Leu	Pro	Phe	Glu	Ala	Arg	Leu	Asn	Ala
			180					185					190		
Ser	Met	Gly	Pro	Gly	Arg	Thr	Val	Val	Val	Lys	Gly	Glu	Val	Asn	Thr
		195					200					205			
Asn	Ala	Thr	Ser	Phe	Asn	Val	Asp	Leu	Val	Ala	Gly	Arg	Ser	Arg	Asp
	210					215					220				
Ile	Ala	Leu	His	Leu	Asn	Pro	Arg	Leu	Asn	Val	Lys	Ala	Phe	Val	Arg
225					230					235					240
Asn	Ser	Phe	Leu	Gln	Asp	Ala	Trp	Gly	Glu	Glu	Glu	Arg	Asn	Ile	Thr
				245					250					255	
Cys	Phe	Pro	Phe	Ser	Ser	Gly	Met	Tyr	Phe	Glu	Met	Ile	Ile	Tyr	Cys
			260					265					270		
Asp	Val	Arg	Glu	Phe	Lys	Val	Ala	Val	Asn	Gly	Val	His	Ser	Leu	Glu
		275					280					285			
Tyr	Lys	His	Arg	Phe	Lys	Asp	Leu	Ser	Ser	Ile	Asp	Thr	Leu	Ala	Val
	290					295					300				
Asp	Gly	Asp	Ile	Arg	Leu	Leu	Asp	Val	Arg	Ser	Trp				
305					310					315					

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTCGGCAC GAGAGCTCTT NTCACAGGAC CAGCCACTAG CGCANCTCGA GCGATGGCCT	60
ATGTCCCCGC ACCGGGCTAC CAGCCACCT ACAACCCGAC GCTGCCTTAC TACCAGCCCA	120
TCCCGGGCGG GCTCAACGTG GGAATGTCTG TTTACATCCA AGGAGTGGCC AGCGAGCACA	180
TGAAGCGGTT CTTCGTGAAC TTTGTGGTTG GGCAGGATCC GGGCTCAGAC GTCGCCTTCC	240
ACTTCAATCC GCGGTTTGAC GGCTGGGACA AGGTGGTCTT CAACACGTTG CAGGGCGGGA	300
AGTGGGGCAG CGAGGAGAGG AAGAGGAGCA TGCCCTTCAA AAAGGGTGCC GCCTTTGAGC	360
TTGGTCTTCA TAGTCCTNGG TTGAGCACTA CAAGGTNGTN GTAAATGGAA TCCCTCTATG	420
ANTAGGGGAC CGNTTTCCTT ANAATTGTAA CCANCTNNAA TTGATGGGNN TCAATTAATN	480

ATCAATTATT GGNGGCANC

499

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGTGGATGGG GATCTGCAAC TTCAATCAAT CAACTTCATC GGAGGCCAGC CCCTCCGGCC	60
CCAGGGACCC CCGATGATGC CACCTTACCC TGGTCCCGGA CATTGCCATC AACAGCTGAA	120
CAGCCTGCCC ACCATGGAAG GACCCCCAAC CTTCAACCCG CCTGTGCCAT ATTTNGGGAG	180
GCTGCAAGGA GGGCTCACAG CTCGAAGAAC CATCATCATC AAGGGCTATG TGCCTCCCAC	240
AGGCAAGAGC TTTGCTATCA ACTTCAAGGT GGGCTCCTCA GGGGACATAG CTCTGCACAT	300
TAATCCCCGC ATGGGCAACG GTACCGTGGT CCGGAACAGC CTTCTTGAAT GGTTCGTGGG	360
GTTNCGAGGA GAAGAAGNTC ACCCACAACC C	391

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 423 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCGGCCCCAG GGACCCCCGA TGATGCCACC TTACCCTGGT CCCGGACATT GCCATCAACA	60
GCTGAACAGC CTGCCCACCA TGGAAGGACC CCCAACCTTC AACCCGCCTG TGCCATATTT	120
CGGGAGGCTG CAAGGAGGGC TCACAGCTCG AAGAACCATC ATCATCAAGG GCTATGTGCC	180
TCCCACAGGC AAGAGCTTTG CTATCAACTT CAAGGTGGGC TCCTCAGGGG ACATAGCTCT	240
GCACATTAAT CCCC GCATGG GCAACGGTAC CGTGGTCCGG AACAGNCTTC TGAATGGCTC	300
GTGGGGATNC GAGGAGAAGG AAGGTCANCC ACAANCCATT TTGTNCCGGA CANTTTTTTT	360
NATCTGTCCA NTTGGTTGTG GTTTGGATCG TTTCAAGGTT TAAGGCAATG GCCAGAACTT	420
TTT	423

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTCGGCAC GAGCACAGGC AAGAGCTTTG CTATCAACTT CAAGGTGGGC TCCTCAGGGG	60
ACATAGCTCT GCACATTAAT CCCCGCATGG GCAACGGTAC CGTGGTCCGG AACAGCCTTC	120
TGAATGGCTC GTGGGGATCC GAGGAGAAGA AGATCACCCA CAACCCATTT GGTCCCGGAC	180
AGTTCTTTGA TCTGTCCATT CGCTGTGGCT TGGATCGCTT CAAGGTTTAC GGCAATGGCC	240
AGCACCTCTT TGACTTTGCC CATCGNCTCT CGGCCTTCCA GAGGGTGGAC ANATTNGAAA	300
TCCAGGGTGA TGTCAACTTG TCCTATGTCC AGATCTAATC TTATTCTTGG GGCCATAATT	360
CATGGGAAAC AGATTATNCN CTAGGGTTCT TTTTATAGGCC CTAATAAAAT GTCTTAGGGG	420
GGTAAAAAAA AAAA	434

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTTCAATCCG CGGTTTGACG GCTGGGACAA GGTGGTCTTC AACACGTTGC AGGGCGGGAA	60
GTGGGGCAGC GAGGAGAGGA AGAGGAGCAT GCCCTTCAAA AAGGGTGCCG CCTTTAAGCT	120
GGTCTTCATA GTCCTGGCTG AGCACTACAA GGTGGTGGTA AATGGAAATC CCTTCTATGA	180
GTACGGGCAC CGGCTTCCCC TACAGATGGT CACCCACCTG CAAGTGGATG GGGATCTNCA	240
ACTTCAATCA ATCAACTTCA TCGGGAGGNC AGCCNTCCG GCCCCAGGGA CCCCCGATGA	300
TGCCACCTTA CCCTGGTNCC GGACATTGGC CATCAGCAGT TGAACAGCTG TCCA	354

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGGTCCGGA ACAGCCTTCT GAATGGCTCG TGGGGATCCG AGGAGAAGAA GATCACCCAC	60
AACCCATTTG GTCCCGGACA GTTCTTTGAT CTGTCCATTC GCTGTGGCTT GGATCGCTTC	120
AAGGTTTACG CCAATGGCCA GCACCTCTTT GACTTTGCCC ATCGCCTCTC GGCCTTCCAG	180
AGGGTGGACA CATTGGAAAT CCAGGGTGAT GTCACCTTGT CCTATGTCCA GATCTAATCT	240
ATTNCTGGGG CCATAACTCA TGGGAAAACA GAATTATCCC CTAGGACTCC TTTCTAAAGC	300
CCNCTAATAA AAANGTCTGA GGGTGTCTC	329

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGGGCTCAA CGTGGGAATG TCTGTTTACA TCCAAGGAGT GGCCAGCGAG CACATGAAGC	60
GGTTCTTCGT GAACTTTGTG GTTGGGCAGG ATCCGGGCTC AGACGTCGCC TTCCACTTCA	120
ATCCGCGGTT TGACGGCTGG GACAAGGTGG TCTTCAACAC GTTGCAGGGC GGGAAGTGGG	180
GCAGCNAGGA GAGGAAGAGG AGCATGCCCT TCAAAAAGGG TGCCGCCTT	229

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 194 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGAAGAGGAG CATGCCCTTC AAAAAGGGTG CCGCCTTTAA CCTGGTNTTC ATAGTCCTGG	60
CTGAGCACTA CAAGGTGGTG GTAAATGGAA ATCCCTTCTA TNAGTACGGG CACCGGCTTC	120
CCCTACAGAT GGTCAACCCAC CTGCAAGTGG ATGGGGATCT GCAACTTCAT TCATTCAACT	180

TCATCGGAGG CCAG

194

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATTCCGTTC TCTACTCCCG CCATCCCACC TATAATGTAC CCCCACCCCG CCTATCCAAT	60
GCCTTTAATC ACCACCATTC TGGGAGGGCT GTACCCATCC AAGTCCATCC TCCTGTAAGG	120
CACTTGCCTG CCCAGTGCTC ANAGGTTCCA CATCAACCTG TGCTCTGGGA AACCACATCG	180
CCTTCCACCT GNAACCCCG TTTTGAATGA GAATGCTGTG GTCCGCAACA CCCAGATNGA	240
CAACTCCTGG GGGTCTGAGG AGCGAAGTGT GCCCCGAAAA ATGCCCTTGG TNCGTGGCCA	300
GAGGTTNTNA GGTGGATCTT GTGTGAAGTT CAATGNGTNC AAGTGGGCCT GGATGGTNAG	360
NANTGTTTGN ATNATTANNC TGGGNTTGNG GNAACTGNCG AANNTTNAAC AGATNGNAGT	420
TGGGGGGGNG ANANTCAGNT GNACCGTTTT GNAGNNATAG GGGGNTTTNT TGGCCTTGGG	480
GGGGGGGGTT GGGGTTTTG	499

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTTTTGCCAA CAAGCATTTT NATTTCTTTA TTTTAAGGAC ACTGGGAAAG GAGCCAGTCC	60
CCTGAAGAGA ACACTCTGGT CAGGTGGTGG AGGCCAGTGG GAAGCCATCA GGCCTGCTTT	120
CCAGGAGGGG TGAAGGGTTG GTGCACGGTG CAAGGTGAGA GTGAAGGTTA AAGGTCAGAG	180
AGGAGGGGCT GAGGAGGCCA CCTTCCACCA GGAGCAGACA GCTGGTGGCT TGGGAAGTGG	240
GGTGGAGCTG CGTGGGGGAT GGGGAAGGGGA CTGAGCATGG GGCTTCATCT TNCAGTCCCC	300
ACTCCTGCCC TCTTCCCTGG CTGTGCCTGC CTNCCTGGGA TGGTAGGGTT TCCANCANTT	360
GGAGGCCCCA NGTGCT	376

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TTCAGATCAC TGTCAATGGG ACCGTTCTCA GCTCCAGTGG AACCAGGTTT NCTGTGAACT 60
TTCAGACTGG CTTCACTGGA AATAACATTG CCTTCCACTT CAACCCTCGG TTTGAAGATG 120
GAGGGTACGT GGTGTGCACA GNAGGCAGAA CGGAAGCTGG GGGCCCGAGG AGAGGAAGAC 180
ACACATGCCT TTCCAGAAGG GGATGCCCTT TAACCTCTGC TTCCTGGTGC AGAGCTCAGA 240
TTTCAAGGTG ATGGTGAACG GGATCCTCTT CGTGCAGTAC TT 282

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGCAGAGCG CCCCTGGACA GATGTNCTCT ACTCCCGCCA TCCCACCTAT GATGTACCCC 60
CACCCCGCCT ATCCGATGCC TTTNAACACC ACCATTCTGG GAGGGCTGTA CCCATCCAAG 120
ATCCATCCTC CTGTCAGGCA CTGTCCTGCC CAGTGCTCAG AGGTTCCACA TCAACCTGTG 180
CTCTGGGAAC CACATCGCCT TCCACCTGAA CCCCCGTTTT GATGAGAATG CTGTGGTCCG 240
CAACACCCAG ATCGACAAAT TCCTGGGGGG TCTT 274

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTTTTGCCAA CAAGCATTTT NATTTCTTTA TTTTAAGGAC ACTGGGAAAG GAGCCAGTCC	60
CCTGAAGAGA ACACTCTGGT CAGGTGGTGG AGGCCAGTGG GAAGCCATCA GGCCTGCTTT	120
CCAGGAGGGG TGAAGGGTTG GTGCACGGTG CAAGGTGAGA GTNAAGGTTA AAGGTCAGAG	180
AGGAGGGGCT GAGGAGGCCA CCTTCCACCA GGAGCAGACA GCTGGTGGCT TGGGAAGTGG	240
GGTGGGAGCT GTCGTNGGGG GATGGNAAGG GGACTGAGCC ATGGGGGCTT TCATCTTNCA	300
CTGCCCCACTC CTGCCCTTTT CCCTGGTTTG TGNCTGNCCT TC	342

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCTGCTTCTG GCTACAGCCA CCNTGGAACG GAGAAGGCAG CTGACGGGGA TTGCCTTCNT	60
CAGCCGCAGC AGCACCTGGG GCTCCAGCTG CTGGAATCNT ACCATCCCAG GAGGCAGGCA	120
CAGCCAGGGA GAGGGGAGGA GTGGGCAGTG AAGATNAAGC CCCATGCTCA GTCCCCCTCC	180
ATCCCCCAGC CAGCTCCACC CCAGTTCCAA GNCACCAGCT GTCTGCTCCT GGTGGGAGGT	240
GGCCTC	246

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGCANAGCAG AGGTGTGGAT CTTNTNTAAA GCTCACTGCC TCAAGGTGGC CGTGGATGGT	60
CAGCACCTGT TTAAATACTA CCATCGCCTG AGGAACCTGC CCACCATCAA CAGACTGGGA	120
GTGGGGGGCG AACATCCAGC TGACCCATGT GCAGACATAG GCGGCTTCCT GGCCCTGGGG	180
CGGGGGCTNA GNTTTGGGGN AGTCTGGGTC CTNTAATNAT CCNCANTT	228

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCCCTCTAC AAAGGACTTC CTAGTGGGTG TNAAAGGCAG CGGTGGCCAC ANAGGCGGCG	60
GAGAGATGGC CTTAGCGGT TCCAGGCTC CCTACCTGAG TCCAGCTGTC CCCTTTTTTG	120
GGACTATTCA AGGAGGTCTC CAGGACGGAC TTCAGATCAC T	161

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCTGTGCAG CTGTCCTACA TCAGCTTCCA GGNNAGACTG TCCACCTGGC ACCGGTNCCA	60
GGGGCGGGGA ATGCGGGGNG NAGCGTAGTT GATACTGAAG NCNCTGATGG GTGGGGCNNA	120
AGNCANATCT CCTNACCCAG GTCACCTCTGG GGGACAACCT CTGGCTTCCC TGTCCCAGTA	180
CCTGGCTGNC NACTTCTCCT CTGTGAATC TGANCCCTCC TTCTGTGTTT ACTGTCTCTG	240
TCCGGAACAA CTGCCTTGGT CTCCCAGANT GCTCAGGTGA CCCTTTNTTN TTTCNACCCT	300
TCAATT	306

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CTCATACAGA GGGCATCGGG TCCCACCCTG TCACTCATTT CATCGTCTAA AATGTAATCA	60
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TGAGTGTTTG CTTGAGCCA GGGACAGTNC TGCTGCAGGG GACCCAGCTG GGACCAAGGC 120
AGACTGTCTC TCCCCTCCTG GGATTACAG GGTGATGGCT CTGAAACATT CTGTAGTGTT 180
CTTTGAACAC GAGTTTTCCC TGGAGATCGC TTTCTGCAGG CCTCTTGGTC CTGACTGTGG 240
CTTCTTTTCA GAGCCTGCCA TTCGCTGCAA GGTGAACAN CCCCATGGGC CCTGGGACGA 300
ACTGTCGTCG TAAAAGGAG AAGTGAATGC AAATGNCCAA AAAGCTTTTA ATGTTTGACC 360
TACTAGCAGG AAATCAAAGG GTATTGCNTC TTACAATTGN ACCCAGGCTG AATATTAAAG 420
CATTTTAAAG AATTCTTTTT CTTCAGGAG 449

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCAATCCTC GTTCAAAAG GGCCGGCTGC ATTGTTTGCA ATACTTTNAT AAATGAAAAA 60
TGGGGACGGG AAGAGATCAC CTATGACACG CCTTTCAAAA GAGAAAAGTC TTTTNAGATC 120
GTAATTATGG TGCTGAAGGA CAAATTCCAG GTGGCTGTAA ATGGAAAACA TACTCTGCTC 180
TATGGCCACA GGATCGGCCC AGAGAAAATA GACACTCTGG GCATTTATGG CAAAGTGAAT 240
ATTCACTCAA TTGGTTTTAG CTTCA 265

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGCCACTCT GCCCTCTCTC CTA CTTTGGC TGACTCTTCA AGAATGCCAT TCAACAAGTA 60
TTTATGGAGT ACCTACTATA ATACAGTAGC TAACATGTAT TGAGCACAGA TTTTTTTTGG 120
TAAAACTGTG AGGAGCTAGG ATATATACTT GGTGAAACAA ACCAGTATGT TCCCTGTTCT 180
CTTGAGCTTC GACTCTTCTG TGCTCTATTG CTGCGCACTG CTTTTTCTAC AGGCATTACA 240
TCAACTCCTA AGGGGTCTCT TGGGGATTAG TTAAGCAGCT ATTTAAATCA CCCGAAGGAC 300

ACTTAATTTA CAGATGACAC AANTCCTTTC CCCAGTGATT CAACTGTTCA TAA

353

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAAACACCAG TTTTTGGGGC CAGTNCCTCA NTTTCAATCC AGGTAACCTT TAANTGAAAC	60
TTGCCTAAAA TTTAGGTCA TACACAGAAG AGACTCCAAT CGACAAGAAG CTGGAAAAGA	120
ATGATGTTGT CCTTAAACAA CCTACAGANT ATCATCTATA ACCCGGTAAT CCCGTTTNTT	180
GGCACCATTC CTGATCAGCT GGATCCTGGA ACTTTGATTG TAATACGTGG GCAT	234

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ACACGCTGGA AATTAATGGA GACATCCACT TACTGGAAGT AAGGNGNTGG TAGCCTACCT	60
ACACAGCTGC TACAAAAACC AAAATACAGA ATGGCTTCTG TGATACTGGC CTTGCTGAAA	120
CGCATCTCAC TGTCATTCTA TTGTTTATAT TGTTAAATG AGCTTGTGCA CCATTAGGTC	180
CTGCTGGGTG TTCTCAGTCC TTGCCATGAA GTATGGTGGT GTCTAGCACT GAATGGGGAA	240
ACTGGGGGCA GCAACACTTA TAGCCAGTTA AAGCCACTCT GCCCTCTCTC CTACTTTGGG	300
CTGACTCTTC AAGAATGCCA TTCAACAAGT ATTTATGGGG TACC	344

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 502 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AATTCGGCAN AGCTTCAAAC CTTTGAGACA TAGTTCATAG GTGGTATTTT GGTGCAAGTC 60
AAAGTGTGAT NGACAGTCGA ATNTTTGCTC TTGGTGTAGA CAGTTCTGGG TGCGATTTTA 120
GAAATGTCTG CTCCTCTATT ACTAGGCTGT NGGGAAACAG TTCTACAGTA AGGAATGGAA 180
TGANATGAAG CTGCCCTCCA CGGTTTAAAC TGTTCATTTT CTATGCAACT TTATAAAATA 240
TTCCACATGA ANTAACCCAG GCAAAAATAC TTCACAGGCT GGGGGGCGTG GCCAGANCTT 300
TGGGAACCTA TTGGGAAAAG GAAACCAAAN CACANCAATG TTTAGAAGGG GGAAGGATTT 360
TTAGTTTATN AATNTGAAGT NTTGGGNNGT TGCTGAGGCT GAGGCCTGGG CCGGNGGCTT 420
GGGGATTGTT TCCNGGTTNC CACTCTGGTG NGGNNTTNCC NGGGCAGTTG GGTGNTTTTA 480
TGACGGGATT GGTATTGTGT TG 502

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGCCCATGGC CTATGTCCCC GCACCG 26

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CGCAAGCTTT TAGATCTGGA CATAGGAC 28

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGCCCATGGC CTTACGCGGT TCCCAG

26

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGCAAGCTTC AGGGTTGGAA AGGCTG

26

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGCCCATGCT GTTGTCTTA AACAAAC

26

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGCCTGCAGC ACAGAAGCCA TTCTG

25

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGCCTGCAGC TATGCAACTT TATAAAATAT TCC

33

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGCCCCGGGG CCTATGTCCC CGCAC

25

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGCGGTACCT TAGATCTGGA CATAGGAC

28

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCGGTACCT TAGATCTGGA CATAGGAC

CGCCCCGGGG CCTTCAGCGG TTCCCAG

27

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGCGGTACCC AGGGTTGGAA AGGCTG

26

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CGCCCCGGGT TGTCTTAAA CAACCTAC

28

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGCGGTACCC ACAGAAGCCA TTCTG

25

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

CGCCCCGGGG CCTTCAGCGG TTCCCAG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGCGGTACCC TATGCAACTT TATAAAATAT TCC

33

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGCCCCGGGG CCATCATGGC CTATGTCCCC G

31

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGCGGTACCT TAGATCTGGA CATAGGAC

28

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGCCCCGGGG CCATCATGGC CTTACGCGGT TC

32

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: cDNA

CGCGGTACCC AGGGTTGGAA AGGCTG

26

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

CGCCCCGGGG CCATCATGAT GTTGTCTTA AAC

33

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

CGCGGTACCC ACAGAAGCCA TTCTG

25